

SEQUENCE LISTING

<110> Virax Development Pty Ltd

<120> A viral vector and methods of using same

<130> 12521330/JEH

<150> AU 2003905642

<151> 2003-10-15

<150> AU 2003905683

<151> 2003-10-16

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<170> PatentIn version 3.1

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<212> .DNA

<213> Human immunodeficiency virus

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<221> CDS

<222> (1)..(1329)

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His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
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Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
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Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
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Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
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Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
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 <213> Human immunodeficiency virus

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His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp
85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Ala Gly Thr Gly Asn Ser Ser
115 120 125

Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met
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Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
145 150 155 160

Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
165 170 175

Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
180 185 190

Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
195 200 205

Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
210 215 220

Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
225 230 235 240

Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
245 250 255

Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
260 265 270

Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
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			20					25					30			
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gat aca gga gca gat gat aca gta tta Asp Thr Gly Ala Asp Asp Thr Val Leu 85 90	gaa gaa atg aat ttg cca gga Glu Glu Met Asn Leu Pro Gly 95		288
aaa tgg aaa cca aaa atg ata ggg gga Lys Trp Lys Pro Lys Met Ile Gly Gly 100 105	att gga ggt ttt atc aaa gta Ile Gly Gly Phe Ile Lys Val 110		336
aga cag tac gat cag ata cct gta gaa Arg Gln Tyr Asp Gln Ile Pro Val Glu 115 120	atc tgt gga cat aaa gct ata Ile Cys Gly His Lys Ala Ile 125		384
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660 665 670	
gtc agt caa ata ata gag cag tta ata aaa aag gaa aag gtc tac ctg	2064
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690 695 700	
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Leu	Lys	Leu	Ala	Gly	Arg	Trp	Pro	Val	Lys	Thr	Ile	His	Thr	Asp	Asn	
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Gly	Ser	Asn	Phe	Thr	Ser	Thr	Thr	Val	Lys	Ala	Ala	Cys	Trp	Trp	Ala	
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gta	gta	gaa	tct	atg	aat	aat	gaa	tta	aag	aaa	att	ata	gga	cag	gta	2640
Val	Val	Glu	Ser	Met	Asn	Asn	Glu	Leu	Lys	Lys	Ile	Ile	Gly	Gln	Val	
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Arg	Asp	Gln	Ala	Glu	His	Leu	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe	
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Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Asp	
		930				935					940					
aac	aaa	gat	ccc	ctt	tgg	aaa	gga	cca	gca	aag	ctt	ctc	tgg	aaa	ggt	2880
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10/23

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Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro							
	965			970		975	
aga aga aaa gca aaa atc att agg gat tat gga aaa cag atg gca ggt							2976
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	980			985		990	
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Val Trp Gly Gly Glu Asn Asn Ser Leu Ser Glu Ala Gly Ala Asp Arg							
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Gln Gly Thr Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg							
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Pro Leu Val Thr Ile Arg Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu							
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Asp Thr Gly Ala Asp Asp Thr Val Leu Glu Glu Met Asn Leu Pro Gly							
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Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
 180 185 190

Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
 195 200 205

Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
 210 215 220

Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
 225 230 235 240

Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
 245 250 255

Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
 260 265 270

Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
 275 280 285

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Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
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Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr
 325 330 335

Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
 340 345 350

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 355 360 365

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Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
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Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val
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Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys
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Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile
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Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile
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